<210>   1
<211>   1760
<212>   DNA
<213>   Glycine max

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tgtacaacta cgaaaccacc gaacttgttc acgagaacag gaatggcacc tatcagtgga 180
ttgtcaaacc caaatctgtc aaatacgaat ttaaaaccaa catccatgtt cctaaattag 240
gggtaatgct tgtgggttgg ggtggaaaca acggctcaac cctcaccggt ggtgttattg 300
ctaaccgaga gggcatttca tgggctacaa aggacaagat tcaacaagcc aattactttg 360
gctccctcac ccaagcctca gctatccgag ttgggtcctt ccaggagag gaaatctatg 420
ccccattcaa gagcctgctt ccaatggtta accctgacga cattgtgttt gggggatggg 480
atatcagcaa catgaacctg ctgatgcca tggccaggc aaaggtgttt gacatcgatt 540
tgcagaagca gttgaggcct tacatggaat ccatgcttcc actccccgga atctatgacc 600
cggatttcat tgctgccaac caagaggagc gtgccaacaa cgtcatcaag ggcacaaagc 660
aagagcaagt tcaacaaatc atcaaagaca tcaaggcgtt taaggaagcc accaaagtgg 720
acaaggtggt tgtactgtgg actgccaaca cagagaggta cagtaatttg gttgtgggcc 780
ttaatgacac catggagaat ctcttggctg ctgtggacag aaatgaggct gagatttctc 840
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ctcagaacac ttttgtacca gggctgattg atcttgccat cgcgaggaac actttgattg 960
gtggagatga cttcaagagt ggtcagacca aaatgaaatc tgtgttggtt gatttccttg 1020
tgggggctgg tatcaagcca acatctatag tcagttacaa ccatctggga aacaatgatg 1080
gtatgaatct ttcggctcca caaactttcc gttccaagga aatctccaag agcaacgttg 1140
ttgatgatat ggtcaacagc aatgccatcc tctatgagcc tggtgaacat ccagaccatg 1200
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cttcagagat attcatgggt ggaaagagca ccattgtttt gcacaacaca tgcgaggatt 1320
ccctcttagc tgctcctatt atcttggact tggtccttct tgctgagctc agcactagaa 1380
tcgagtttaa agctgaaaat gagggaaaat tccactcatt ccacccagtt gctaccatcc 1440
tcagctacct caccaaggct cctctggttc caccgggtac accagtggtg aatgcattgt 1500
caaagcagcg tgcaatgctg gaaaacataa tgagggcttg tgttggattg gccccagaga 1560
ataacatgat tctcgagtac aagtgaagca tgggaccgaa gaataatata gttggggtag 1620
cctagctgaa tgttttatgt taataatatg tttgcttata attttgcaag tgtaattgaa 1680
tgcatcagct tcattaatgc tttagagcgg ggcatattct gtttactagg aacatgaatg 1740
aatgtagtat aattttgtgt   1760

<210>   2
<211>   510
<212>   PRT
<213>   Glycine max

<400> 2

```
Met Phe Ile Glu Asn Phe Lys Val Glu Cys Pro Asn Val Lys Tyr Thr
 1               5                  10                  15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
                20                  25                  30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
        35                  40                  45

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
    50                  55                  60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65                  70                  75                  80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
            85                  90                  95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
            100                 105                 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
    115                 120                 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
    130                 135                 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145                 150                 155                 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
            165                 170                 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
            180                 185                 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
            195                 200                 205

Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
    210                 215                 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225                 230                 235                 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
            245                 250                 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
            260                 265                 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
    275                 280                 285

Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
    290                 295                 300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
305                 310                 315                 320

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
            325                 330                 335
```

2

```
His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
        340             345             350
Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
        355             360             365
Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
    370             375             380
Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385             390             395             400
Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
            405             410             415
His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
            420             425             430
Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
        435             440             445
Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
        450             455             460
Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465             470             475             480
Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
            485             490             495
Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
            500             505             510

<210>  3
<211>  35
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: synthetic oligonucleotide

<400>  3
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<210>  4
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: synthetic oligonuclotide

<400>  4
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<210>  5
<211>  1533
<212>  DNA
<213>  Glycine max

<400>  5
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cagtccgtgt acaactacga aaccaccgaa cttgttcacg agaacaggaa tggcacctat  120
cagtggattg tcaaacccaa atctgtcaaa tacgaattta aaaccaacat ccatgttcct  180
aaattagggg taatgcttgt gggttggggt ggaaacaacg gctcaaccct caccggtggt  240
gttattgcta accgagaggg catttcatgg gctacaaagg acaagattca acaagccaat  300
```

3

```
tactttggct ccctcaccca agcctcagct atccgagttg ggtccttcca gggagaggaa  360
atctatgccc cattcaagag cctgcttcca atggttaacc ctgacgacat tgtgtttggg  420
ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac  480
atcgatttgc agaagcagtt gaggccttac atggaatcca tgcttccact ccccggaatc  540
tatgacccgg atttcattgc tgccaaccaa gaggagcgtg ccaacaacgt catcaagggc  600
acaaagcaag agcaagttca acaaatcatc aaagacatca aggcgtttaa ggaagccacc  660
aaagtggaca aggtggttgt actgtggact gccaacacag agaggtacag taatttggtt  720
gtgggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag  780
atttctcctt ccaccttgta tgccattgct tgtgttatgg aaaatgttcc tttcattaat  840
ggaagccctc agaacacttt tgtaccaggg ctgattgatc ttgccatcgc gaggaacact  900
ttgattggtg gagatgactt caagagtggt cagaccaaaa tgaaatctgt gttggttgat  960
ttccttgtgg gggctggtat caagccaaca tctatagtca gttacaacca tctgggaaac 1020
aatgatggta tgaatctttc ggctccacaa actttccgtt ccaaggaaat ctccaagagc 1080
aacgttgttg atgatatggt caacagcaat gccatcctct atgagcctgg tgaacatcca 1140
gaccatgttg ttgttattaa gtatgtgcct tacgtagggg acagcaatag agccatggat 1200
gagtacactt cagagatatt catgggtgga aagagcacca ttgttttgca caacacatgc 1260
gaggattccc tcttagctgc tcctattatc ttggacttgg tccttcttgc tgagctcagc 1320
actagaatcg agtttaaagc tgaaaatgag ggaaaattcc actcattcca cccagttgct 1380
accatcctca gctacctcac caaggctcct ctggttccac cgggtacacc agtggtgaat 1440
gcattgtcaa agcagcgtgc aatgctggaa aacataatga gggcttgtgt ggattggcc 1500
ccagagaata acatgattct cgagtacaag tga                               1533
```

<210> 6
<211> 510
<212> PRT
<213> Glycine max

<400> 6

```
Met Phe Ile Glu Asn Phe Lys Val Glu Cys Pro Asn Val Lys Tyr Thr
 1               5                  10                  15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
           20                  25                  30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
       35                  40                  45

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
   50                  55                  60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
 65                  70                  75                  80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
               85                  90                  95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
               100                 105                 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
           115                 120                 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
       130                 135                 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145                 150                 155                 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
               165                 170                 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
           180                 185                 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
       195                 200                 205
```

4

```
Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
    210             215             220
```

```
Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225             230             235             240
```

```
Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
                245             250             255
```

```
Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
                260             265             270
```

```
Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
        275             280             285
```

```
Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
    290             295             300
```

```
Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
305             310             315             320
```

```
Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
                325             330             335
```

```
His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
            340             345             350
```

```
Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
        355             360             365
```

```
Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
    370             375             380
```

```
Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Asn Arg Ala Met Asp
385             390             395             400
```

```
Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
                405             410             415
```

```
His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
            420             425             430
```

```
Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
        435             440             445
```

```
Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
    450             455             460
```

```
Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465             470             475             480
```

```
Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
                485             490             495
```

```
Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
            500             505             510
```

<210> 7
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

5

<400>   9

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atgttcatcg agaatttta  ggttgagtgt cctaatgtga agtacaccga gactgagatt   60
cagtccgtgt acaactacga aaccaccgaa cttgttcacg agaacaggaa tggcacctat  120
cagtggattg tcaaacccaa atctgtcaaa tacgaattta aaaccaacat ccatgttcct  180
aaattagggg taatgcttgt gggttggggt ggaaacaacg gctcaaccct caccggtggt  240
gttattgcta accgagaggg catttcatgg gctacaaagg acaagattca acaagccaat  300
tactttggct ccctcaccca agcctcagct atccgagttg ggtccttcca gggagaggaa  360
atctatgccc cattcaagag cctgcttcca atggttaacc ctgacgacat tgtgtttggg  420
ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac  480
atcgatttgc agaagcagtt gaggccttac atggaatcca tgcttccact ccccggaatc  540
tatgacccgg atttcattgc tgccaaccaa gaggagcgtg ccaacaacgt catcaagggc  600
acaaagcaag agcaagttca acaaatcatc aaagacatca aggcgtttaa ggaagccacc  660
aaagtggaca aggtggttgt actgtggact gccaacacag agaggtacag taatttggtt  720
gtgggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag  780
atttctcctt ccaccttgta tgccattgct tgtgttatgg aaaatgttcc tttcattaat  840
ggaagccctc agaacacttt tgtaccaggg ctgattgatc ttgccatcgc gaggaacact  900
ttgattggtg gagatgactt caagagtggt cagaccaaaa tgaaatctgt gttggttgat  960
ttccttgtgg gggctggtat caagccaaca tctatagtca gttacaacca tctgggaaac 1020
aatgatggta tgaatctttc ggctccacaa actttccgtt ccaaggaaat ctccaagagc 1080
aacgttgttg atgatatggt caacagcaat gccatcctct atgagcctgg tgaacatcca 1140
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gagtacactt cagagatatt catgggtgga aagagcacca ttgtttttgca caacacatgc 1260
gaggattccc tcttagctgc tcctattatc ttggacttgg tccttcttgc tgagctcagc 1320
actagaatcg agtttaaagc tgaaaatgag ggaaaattcc actcattcca cccagttgct 1380
accatcctca gctacctcac caaggctcct ctggttccac cgggtacacc agtggtgaat 1440
gcattgtcaa agcagcgtgc aatgctggaa aacataatga gggcttgtgt tggattggcc 1500
ccagagaata acatgattct cgagtacaag tga                                1533
```

<400>   10

```
Met Phe Ile Glu Asn Phe Lys Val Glu Cys Pro Asn Val Lys Tyr Thr
  1               5                  10                  15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
              20                  25                  30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
          35                  40                  45

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
      50                  55                  60
```

6

```
Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
 65           70              75           80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
             85              90              95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
            100             105             110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
        115             120             125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
    130             135             140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145             150             155             160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
            165             170             175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
        180             185             190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
        195             200             205

Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
    210             215             220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225             230             235             240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
            245             250             255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
            260             265             270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
    275             280             285

Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
    290             295             300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
305             310             315             320

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
            325             330             335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
            340             345             350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
        355             360             365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
    370             375             380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385             390             395             400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
            405             410             415
```

                                    7

```
His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
          420             425             430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
          435             440             445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
    450             455             460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465             470             475             480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
              485             490             495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
          500             505             510
```

```
<210>   11
<211>   1533
<212>   DNA
<213>   Glycine max
```

```
<400>   11
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cagtggattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca  180
aaattggggg tgatgcttgt gggttggggt ggaaacaacg gctctaccct caccggtggt  240
gttattgcta acagagagga catttcatgg gctacaaagg acaagattca acaagccaat  300
tactttggct ccctcaccca agcctcagct attcgagttg gatccttcca gggagaggaa  360
atctatgccc cattcaagag tctgcttcca atggttaatc ctgacgacat tgtgtttggg  420
ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac  480
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tacgacccgg atttcattgc tgccaaccaa gaggagcgtg ccaacaacgt gattaaggc  600
acaaagcaag agcaagttca gcaaatcatc aaagacatca aggcgtttaa ggaagccacc  660
aaagtggaca aggtggttgt cctgtggact gccaacacag agaggtatag caatttggtt  720
gtaggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag  780
atttctcctt ccaccttgta tgccattgcc tgtgtgatgg aaaatgttcc tttcattaat  840
ggaagccctc agaacacttt tgtaccaggg ctgattgatc ttgccatcgc gaggaacact  900
ttgattggtg gagatgactt caagagtggt cagaccaaaa tgaaatctgt gttggttgat  960
tttcttgtgg gggctggtat caagccaaca tctatagtta gttacaacca tctgggaaac 1020
aatgatggta tgaatctctc ggctccacaa accttccgct ccaaggaaat ctccaagagc 1080
aacgttgttg acgatatggt caacagcaat gccatcctct atgagcctgg tgaacatccc 1140
gaccatgttg ttgttattaa gtatgtgcct tacgtagggg atagcaagag agccatggat 1200
gagtacactt cagagatatt catgggtgga aagaacacca ttgtttttgca caacacatgt 1260
gaggattccc ttttagctgc tcctattatc ttggacttgg tccttcttgc tgagctgagc 1320
actagaatcc agtttaaagc tgaaaatgag ggaaaattcc actcattcca cccagttgct 1380
accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtggtgaat 1440
gcattgtcaa agcagcgtgc aatgctggaa aacataatga gggcttgtgt tggattggcc 1500
ccagagaata acatgattct cgagtacaag tga                              1533
```

```
<210>   12
<211>   510
<212>   PRT
<213>   Glycine max
```

```
<400>   12
Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
  1               5              10              15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
          20              25              30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
          35              40              45
```

8

```
Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
    50              55              60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65              70              75              80

Val Ile Ala Asn Arg Glu Asp Ile Ser Trp Ala Thr Lys Asp Lys Ile
            85              90              95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
            100             105             110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
        115             120             125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
    130             135             140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145             150             155             160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
            165             170             175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
            180             185             190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
        195             200             205

Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
    210             215             220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225             230             235             240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
            245             250             255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
            260             265             270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
    275             280             285

Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
    290             295             300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
305             310             315             320

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
            325             330             335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
            340             345             350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
    355             360             365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370             375             380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385             390             395             400
```

9

```
Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
            405              410              415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
            420              425              430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
            435              440              445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
    450              455              460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465              470              475              480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
            485              490              495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
            500              505              510
```

```
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<211>  1533
<212>  DNA
<213>  Glycine max

<400>  13
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cagtggattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca   180
aaattggggg tgatgcttgt gggttggggt ggaaacaacg gctctaccct caccggtggt   240
gttattgcta acagagaggg catttcatgg gctacaaagg acaagattca acaagccaat   300
tactttggct ccctcaccca agcctcagct attcgagttg gatccttcca gggagaggaa   360
atctatgccc cattcaagag tctgcttcca atggttaatc ctgacgacat gtgtgtttgg g   420
ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac   480
atcgatttgc agaagcagtt gaggccttac atggaatcca tggttccact ccccggaatc   540
tacgacccgg atttcattgc tgccaaccaa gaggagcgtg ccaacaacgt gattaagggc   600
acaaagcaag agcaagttca gcaaatcatc aaagacatca aggcgtttaa ggaagccacc   660
aaagtggaca aggtggttgt cctgtggact gccaacacag agaggtatag caatttggtt   720
gtaggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag   780
atttctcctt ccaccttgta tgccattgcc tgtgtgatgg aaaatgttcc tttcattaat   840
ggaagccctc agaacacttt tgtaccaggg ctgattgatc ttgccatcgc gaggaacact   900
ttgattggtg gagatgactt caagagtggt cagaccaaaa tgaaatctgt gttggttgat   960
tttcttgtgg gggctggtat caagccaaca tctatagtta gttacaacca tctgggaaac  1020
aatgatggta tgaatctctc ggctccacaa accttccgct ccaaggaaat ctccaagagc  1080
aacgttgttg acgatatggt caacagcaat gccatcctct atgagcctgg tgaacatccc  1140
gaccatgttg ttgttattaa gtatgtgcct tacgtagggg atagcaagag agccatggat  1200
gagtacactt cagagatatt catgggtgga aagaacacca ttgtttttgca caacacatgt  1260
gaggattccc ttttagctgc tcctattatc ttggacttgg tccttcttgc tgagctgagc  1320
actagaatcc agtttaaagc tgaaaatgag ggaaaattcc actcattcca cccagttgct  1380
accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtggtgaat  1440
gcattgtcaa agcagcgtgc aatgctggaa aacataatga gggcttgtgt tggattggcc  1500
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```

```
<210>  14
<211>  510
<212>  PRT
<213>  Glycine max

<400>  14
Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
    1              5              10              15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
            20              25              30
```

```
His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
        35                  40                  45

Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
    50                  55                  60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65                  70                  75                  80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
                85                  90                  95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
            100                 105                 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
        115                 120                 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
    130                 135                 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145                 150                 155                 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
            165                 170                 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
            180                 185                 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
        195                 200                 205

Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
    210                 215                 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225                 230                 235                 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
            245                 250                 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
            260                 265                 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
    275                 280                 285

Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
    290                 295                 300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
305                 310                 315                 320

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
            325                 330                 335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
            340                 345                 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
    355                 360                 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
    370                 375                 380
```

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```
Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385             390             395             400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
            405             410             415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
            420             425             430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
            435             440             445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
        450             455             460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465             470             475             480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
            485             490             495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
            500             505             510
```

```
<210>   15
<211>   1533
<212>   DNA
<213>   Glycine max

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cagtggattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca   180
aaattggggg tgatgcttgt gggttggggt ggaaacaacg gctctaccct caccggtggt   240
gttattgcta cagagagggg catttcatgg gctacaaagg acaagattca acaagccaat   300
tactttggct ccctcaccca agcctcagct attcgagttg gatccttcca gggagaggaa   360
atctatgccc cattcaagag tctgcttcca atggttaatc ctgacgacat tgtgtttggg   420
ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac   480
atcgatttgc agaagcagtt gaggccttac atggaatcca tggttccact ccccggaatc   540
tacgacccgg atttcattgc tgccaaccaa gaggagcgtg ccaacaacgt gattaagggc   600
acaaagcaag agcaagttca gcaaatcatc aaagacatca aggcgtttaa ggaagccacc   660
aaagtggaca aggtggttgt cctgtggact gccaacacag agaggtatag caatttggtt   720
gtaggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag   780
atttctcctt ccaccttgta tgccattgcc tgtgtgatgg aaaatgttcc tttcattaat   840
ggaagccctc agaacacttt tgtaccaggg ctgattgatc ttgccatcgc gaggaacact   900
ttgattggtg gagatgactt caagagtggt cagaccaaaa tgaaatctgt gttggttgat   960
tttcttgtgg gggctggtat caagccaaca tctatagtta gttacaacca tctgggaaac  1020
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aacgttgttg acgatatggt caacagcaat gccatcctct atgagcctgg tgaacatccc  1140
gaccatgttg ttgttattaa gtatgtgcct tacgtagggg atagcaagag agccatggat  1200
gagtacactt cagagatatt catgggtgga aagaacacca ttgtttttgca caacacatgt  1260
gaggattccc ttttagctgc tcctattatc ttggacttgg tccttcttgc tgagctgagc  1320
actagaatcc agtttaaagc tgaaaatgag ggaaaattcc actcattcca cccagttgct  1380
accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtggtgaat  1440
gcattgtcaa agcagcgtgc aatgctggaa aacataatga gggcttgtgt tggattggcc  1500
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```

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<210>   16
<211>   510
<212>   PRT
<213>   Glycine max

<400>   16
Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
 1               5               10              15
```

```
Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
            20              25                    30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
        35              40                    45

Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
    50                  55                    60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65                  70                    75                    80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
                85              90                    95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
            100             105                   110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
        115                 120                   125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
    130                 135                   140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145                 150                   155                   160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
            165                 170                   175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
            180                 185                   190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
        195                 200                   205

Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
    210                 215                   220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225                 230                   235                   240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
            245                 250                   255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
            260                 265                   270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
        275                 280                   285

Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
    290                 295                   300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
305                 310                   315                   320

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
            325                 330                   335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
            340                 345                   350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
        355                 360                   365
```

13

```
Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
    370                 375             380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385                 390             395                     400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
            405             410                     415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
            420             425             430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
        435             440                 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
    450             455                 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465                 470             475                     480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
            485             490                     495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
        500             505             510
```